045 2801 TGTGCAAAAĞATGGTGTAAÂGGAGAGAAGAAGATGTTAGGGAATGTTTGGTGAAAAATATAAATGTAÄGGGGGGAGTĀTCTGAAGGAĞCATGCAGCTĞ CysalalysaspProvatlysGluargargatahisalaargGlucysLeuvallysasnileAsnvatargargGlutyrLeuLysGluHisalaalav 2901 3001 TTAGTGAAAÄATTATTGTCŤCTTCTACCAČAGTATGTTGŤTCCATATACÄATTCACCTTŤTGGCACATGÄCCCAGATTAŤGTCAAAGTAČAGGATATTGÄ alSerGlulysLculeuser, culeuroglutyrvalvalprotyrthrileHisLculeuAlaHisAspproAspTyrvallysvalGlnAspIleGl 1012 ACAACTTAAÄGATGTTAAAĞAATGTCTTTĞGTTTGTTCTĞGAAATATTAATGGCTAAAAÄTGAAAATAACAGTCACGCTTTTATCAGAAĞGATGGTAGAÄ UĞINLEDİYSASPVƏLLYSGLUCYSLEUTTPPhcValleUĞLULLELMCTALBLYSASTIGLUASTASTISETHİSALƏPHELLEAFGLYSKETVBLĞLU 1045 3101 AATATTANAČANACANAGÅTGCCCANGGÄCCAGATGATGCANANATGAÄTGANANGTGTACACTGTGTGTGATGTTGCCATGATATČATGATGTCAÂ ASNI LeLysglinthrlysaspalaglinglypronspaspalalysherasnglulysleutyrthrvalCysaspvalalaHetAsnileileHetScri 1079 3201 AGAGTACTACATACAGTTTĞCAATCTCCTÄAAGACTCGTACTACCAGCTCGTTTCTTCACTCAACCTGGACAAGAATTTCAGTAACACCTAAAAATTATCT ysserThrThrTyrSerLeuGluscrProLysAspProValLouProAlgargPhePheThrGlnProAspLysAsnPheSerAsnThrLysAsnTyrLe .1112 3301 GCCTCCTGLÂATGAATCAŤTTTTCACTCČTĞGAAACCŤAAACAACCÁATGTTCTAGĞAGCTGTTAAĆAAGCCACTTŤCATCAGCAGĞCAAGCAATCŤ UPT-FTGĞİLTCCLYSOTP-OPHOINTPTTGİYLYSPTOLYSTNTİNTAGTVALLEUGİYALƏVƏLASNLYSPTOLEUGOTSETÄLƏĞİYİYSĞİNSET 3401 CAGACCAAAŤCATCACGAAŤGGIAACTGTÄAGCAATGCAÄGCAGCAGCTČAAATGCAAGČTCTCCTGGAÄGAATAAAGCĜGAGGCTTGAŤAGTTCTGAAÄ GlnThrLysSerSerArgMetGluThrValSerAsnAlaSerSerSerSerAsnProSerSerProGlyArglleLysGlyArgleuAspSerSerGluM 3501 TGGATCACAĞTGAAAATGAÂĞATTACACAÂTGTCTTCACCTTTGCCGGGĞAAAAAAAGTĞACAAGAĞACGACTCTGAŤCTTGTAAGGTCTCAATTĞGÂ etAspHisSerGluasnGluaspTyrThrHctserSerProLeuProGlyLysLysSerAspLysArgAspAspSerAspLeuValArgSerGluLeuGl 1212 3601 GAAGCCTAGÁGGCAGGAAAÁAAACGCCCGŤCACAGAACAĠGAGGAGAAAŤTAGGTATGGÁTGACTTGACŤAAGTTGGTAČACGAACAGAÁACCTAAAGGĊ ULysProArgGlyArgLysThrProValThrGluGluGluGluGluGlysLeuGlyHetAspAspLeuThrLysLeuValGlüGlüGlüGlüLysProLysGly 41 1245 3701 AGTEAGEGNÁGTEGGNANAGAGGEERATACÉGETTENGANŤETGNTGNACÁGEAGTEGECŤGNGGNANAGÁGGETENANGÍAGNTATATTÁGNNATGNAG SerGlnárgSernrglysnagglymisthrálasérGluserAspGluGlnGlnTrpProGluGluLysngLeuLysGluAspIleLeuGluAsnGlüA 3801 1279 1312 3901 AAAACGAAGČAAAAAAAŤCTGGACETEČAGGACEAGAĞGAGGAGGAAĞAAGAAGAAĞACAAAGTGGÂAATACGGAACAGAGTCCAÂAAGCAAACAĞ SLysGlySerlysLysLenglyProProAlaProGluGluGluGluGluGluGluGluGluArgGluSerGlyAsnThrGluGluLysSerLysSerLysGlo 1345 100ي CACCGAGTGTCAAGGAGAGCACAGCACAGÁGCAGAATCTCCTGAATCTAGTGCAAYTGAÁTCCACACAGTCCACACCACAGCAGAAAGGACGÁGGAAAGAACCCAT HisangvalSchangangalaglnginangalaglusenproglusenschalaileglusenthrGinsenthrProglnLysglyArgGlyArgPros **4**101 1379 CAMANACISCÉNTENCENTENCAMACIANAMANANTGYGTÁNGTTGYNAMÍNTTNENTTTÉNAMECANTTÍCHANTTNÍTGCHAMAGTÍCCTAMATTTĞ eFLywintproserficprosergicpro 4201 1391 TAAACATACÁTATTGCTGT<u>ÄTTTA</u>AATTGČATAT<u>ATTTA</u>ĞCCCCCATTACÁCTAGGTACGĞCGGCGAAGTĞCTAAAAGGGÁACGGCGATGÄACAAATGTAÄ =<u></u>301 TTAATAACTÝTETETGTGAÄAGETTTGGAÄAAATCTTTTŤTTTTTTTTTTTTTTTTGGŤCAAGCTTGAĞGETGAATAAÄGCETTTGATĞCACAAAATGĞ 4401 CACTGCTGAÂGAGTGGACAĞTTGGACCTTĂCTTTGGTGAĈCCCATACATŤTGTGGTCACÃTGCTTTAGCĈATACAGATGĞTAACATTGAČTATGCAGTCŤ 4501 TETERANAGTÉTANTETECCIÁTESCTATETÁENCATANAGÂNEMANCTTEŤANATATCTTŤTTTCTTTŤTTNATETTTČTENTTTCTEÑASTECTTETÂ 4601 TAGCTTTTAŤCTGCGGCTTŤAAACTGACAĞTACCCGACTĞTTTATTGGAŤCTATTGATTŤGAAAGAATŤTGTTAGGATĀGATCTTAAGČAGTAATCTGŤ 4701 CAGTGTTTGTATTTTCTGCAATTTTACTGTGAAAAAAATTTGTTTTCAACAATTGGTGTCATTTTCTTGATGTCACTATTTGTTGGAGAGTTĀ 4801 4901 AATGGTCTCŤTCCCTTTGTĞTATCTTACCŤAGTGTTTACŤCCTGGGCACČCTTAATCTTČAGAGGTGCTĀAATTGTCTGČCATTACACCÂGAAGGATGCČ 5001 TCTGATAGGÂGGACAACCAŤGCAAATTGTĜAAATAGTCCTGAAGTTCTTĞGATTACTTTÂCACCTCAGTÂTTGATTTGTĈCCAGAATTTŤCTGGCCTTTĈ 5101 ATGGCAATGÄAAATTTTAAĞAACAAAGATTTAAAGTATTTTAATYTTAAĞGAGTGTGTTÄTAAAATAATĞTACTGAATTĈTTTATCCCATTTATCATCĈ 

LYLNLALHLASDFFLKHPGKDVRLLVACCLADIFRIYAPEAPYTSPDKLKDIFMFITRQLKGL

277

196
217
241
LDTVLVNLVPAHKNLNKQAYDL
LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQL

355
375
404

LGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYL
VTAAKKDILLVNDHLLNFVRERTLDKRWRV

FIG. 2

Subdomain III	α-helix C (x x x x E x x x)	489	VKALN E MANC.	TLALN E RIML (bARKI) YTRVR E IKFI (SMEI)							- (\)	······································	
Subdomain II	β-strand 3	(x x x K x x x) 472	ERM K CLYYLYA	YAM K CLKKDVI (CEIFAI) YAM K CLDKKRI (bARKI) YAM K CLDKKRI (DMGPRKI) VAI K CIAKKAL (CamKI)			Subdomain VIa	α-helix E	733	DDEKIRKQ.LEVL		ADQLNIAKQISAG (TORRIK) ESVIMYTKQLLL (NPK1)	
	8-strand 2		ERIF	LLYBLMD (YKIS16) YLGEQVS (PKN2) YLCLCLN (BCK1)			Subdomain V		α-nelly D	540 gkaqdfmkk	GNLQNFLKL (Let23)	GNLQEYLTR	
Subdomain I	nool exists: 1 of the	Mg-ATP binding loop (G x G x x G x V) 426 GKDAAKQI GeDrfGkV (Ror2) GsGsfGdI (CKla) AeGesHiS (Ypka) HeSdfSeV (Mikl)					Subc		β-strand 5	525 IFSK.VMV	LFSCLVME	KFSCLVME (U11a) KFSCLVME (ZmPPK)	
<b>.</b> .		β-strand l	419 YALQ.SA	YTLGVSA (Elm1) YALLNLL (Tsl) YHLKQNI (Cdc15) VKI,VRKI (CK1a)	IVLQESI (Alk5)		Subdomain IV		β-strand 4	509	LEDLINQP (TPCKII)		LVKLIGYC (AFN.)
Hank's conserved		us: sition:		Similar protein kinase sequences:		Hank's conserved regions:			Consensus:	AS3 position:	AS3 sequence:	protein kinase sequences:	

FIG. 3

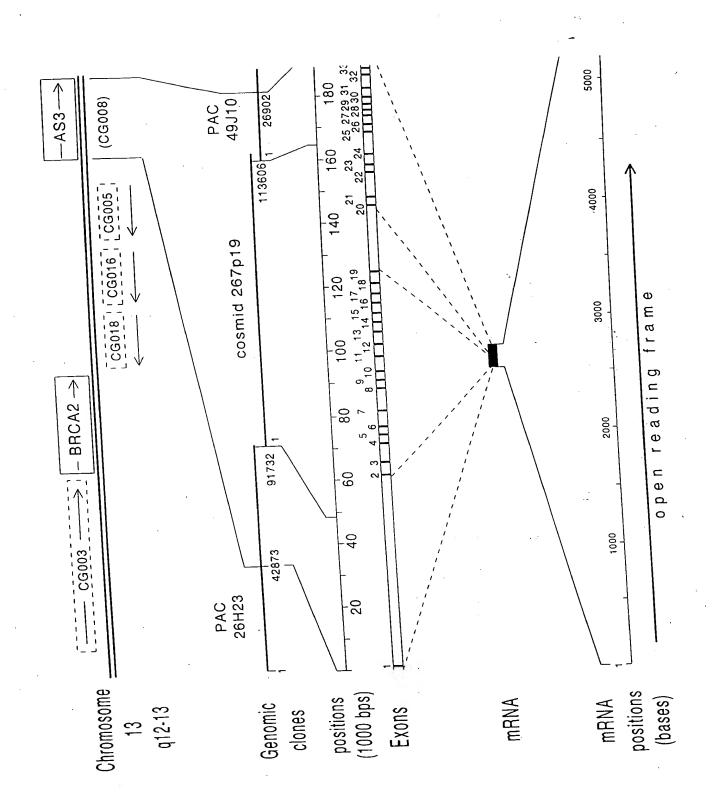


FIG. 4

CCGGAGAG Exon 1ACCCGGAG * 1998
ttttcttg:ttcag * GGGTAGAA Exon 2GATTAAAG * gcgagta
(16397) 174 377 (16602)tttatttttgtatag * ATGGTTGT Exon 3AACTAAAG * gcaagta
(22832) 378 464 (22920) tctttttttatttaag * GATATATT Exon 4TACTTGAG * gtaagca
(23028) 465 562 (23125)ccttatttttag * AACATTGC Exon 5GTTATAAA * gtaagtt
(23747) 563 689 (23873)ttttgaattgcag * CAATGGCC Exon 6CTCATAAG * gtgagta
(32357) 690 854 (32439)tttatgtttttcag * AATITAAA Exon 7TTACCACT * gtaagtc
(37809) 855 911 (37951)ctttctcctcaaaag * TTTTTTAA Exon 8AATTAAAG * gtaactt
(40437) 912 1027 (40554)ttttattttag * AGCAATGA Exon 9TTGGGCAG * gtatatg
(43428) 1028 1122 (43524)tttatattttatcag * GTTTAATG Exon 10CTTAACAG * gtactat
(48471) 1123 1268 (48617) tgttatctttcag * AGTATCTT Exon 11ACAAACGA * gtaagta
(51727) 1269 1420 (51880)tttttgttttaag * TGGAGAGT Exon 12GATGATCG * gtaagtt
(53049) 1421 1534 (53164)tctgcttttttgtag * ACTACTTG Exon 13GCTGTGAA * gtatgtt
(58816) 1535 1616 (58898)tttgtgtttttcag * AGCATTGA Exon 14AACCCAAA * gtaagta
(61447) 1617 1665 (61497)ttgtgtgtatttacag * ACAGATGC Exon 15TATTACAA * gtaagtt
(64323) 1666 1805 (64464)tttattttaag * GAAATTTA Exon 16GITGTGTG * gtaagga
(65916) 1806 1921 (66033) taatctgtattacag * CGTGAAAT Exon 17TCTATCAG * gtatttg
(71527) 1922 2027 (71633)ttggtcatattttag * TGCTCTTA Exon 18TGCTTAAG * gtaagta
(74539) 2028 2188 (74700)tgattcattttatag * GTACTCTC Exon 19ATCAGATC * gtgagtt
(96694) 2189 2312 (96818)ttttttttaatag * AGCCTTGC Exon 20TATTTGAG * gtaatga
(99765) 2313 2471 (99925)tcccctcattttcag * CCTCTGCA Exon 21ATGATCGG * gtaattt
(105674) 2472 2540 (105744)ctcgtttattttag * CTTCCAGG Exon 22TGGTCAAA * gtgagta
(107185) 2541 2677 (107322)ttgtctcttaaatag * ATTCAGGC Exon 23AAAATTAG * gtatgca
(110571) 2678 2801 (110696)ctactcatttttcag * TAAACCAG Exon 24CTATCAAC * gtaagga
[4319] 2802 3006 [4524]ttgtgtctttacag * GATGAATG Exon 25IGTTAGTG * gtaagca
[6829] 3007 3121 [6945]ttttctttttcag * AAAAATTA Exon 26GTTAAAGA * gtaagac
[9074] 3122 3254 [9208]tttttttttttag * ATGTCTTT Exon 27TGAATGAA * gtatgta
[9522] 3255 3374 [9642]tatactattgcag * AAACTGTA Exon 28CTGACAAG * gtagtta
[10614] 3375 3437 [10679ttctcttggttgtag * AATTTCAG Exon 29CTGGAAAA * gtatgtt
[11561] 3438 3583 [11709]catttctcatttcag * CCTAAAAC Exon 30AAGGGGAG * gtaagtg
[15476] 3584 3689 [15583]tgtctgtattaaaag * GCTTGATA Exon 31TTGTAAGG * gtgagat
[21107] 3690 tttttttcccctag * TCTGAATT Exon 32CAGCAGAG * gtaagca
[21640] 4130 4354 [21866]tcttccccaaagcag * AGCAGAAT Exon 33TACACTAG * gtaagat
[26002] 4355 5253 [26902]ctttccttttaag * GTACGGCG Exon 34GAATGAGT * (poly-A)

ili.

TGAGCGGAGTAGCGAGTCGGCAACCCGGAGGGGTAGAAATATTTCTGTCATGGCTCATTCAAAGACTAGGACCAATGATGGAAAAATTACATATCCGCCT 101 MetAlaHisSerLysThrArgThrAsnAspGlyLysIleThrTyrProPro 17 GGGGTCAAGGAAATATCAGATAAAATATCTAAAGAGGAGATGGTGAGACGATTAAAGATGGTTGTGAAAACTTTTATGGATATGGACCAGGACTCTGAAG 201 GlyValLysGluIleSerAspLysIleSerLysGluGluMetValArgArgLeuLysMetValValLysThrPheMetAspMetAspGlnAspSerGluG 51 301 luGluLysGluLeuTyrLeuAsnLeuAlaLeuHisLeuAlaSerAspPhePheLeuLysHisProGlyLysAspValArgLeuLeuValAlaCysCysLe TGCTGATATTTTCAGGATTTATGCTCCTGAAGCTCCTTACACATCCCCTGATAAACTAAAGGATATATTTATGTTTATAACAAGACAGTTGAAGGGGGCTA uAlaAspIlePheArgIleTyrAlaProGluAlaProTyrThrSerProAspLysLeuLysAspIlePheMetPheIleThrArgGlnLeuLysGlyLeu 117 501 151 ATGAAATTTTCACCCAGCTATACAGAACCTTATTTTCAGTTATAAACAATGGCCACAATCAGAAAGTCCATATGCACATGGTAGACCTTATGAGCTCTAT snGluIlePheThrGlnLeuTyrArgThrLeuPheSerValIleAsnAsnGlyHisAsnGlnLysValHisMetHisMetValAspLeuMetSerSerIl 184. eIleCysGluGlyAspThrValSerGlnGluLeuLeuAspThrValLeuValAsnLeuValProAlaHisLysAsnLeuAsnLysGlnAlaTyrAspLeu 217 GCAAAGGCTTTACTGAAGAGGACAGCTCAAGCTATTGAGCCATATATTACCACTTTTTTTAATCAGGTTCTGATGCTTGGGAAAACATCTATCAGCGATT AlaLysAlaLeuLeuLysArgThrAlaGlnAlaIleGluProTyrIleThrThrPhePheAsnGlnValLeuMetLeuGlyLysThrSerIleSerAspL 901 euSerGluHisValPheAspLeuIleLeuGluLeuTyrAsnIleAspSerHisLeuLeuLeuSerValLeuProGlnLeuGluPheLysLeuLysSerAs 284 TGATAATGAGGAGCGCCTACAAGTTGTTAAACTACTGGCAAAAATGTTTGGGGCAAAGGATTCAGAATTGGCTTCTCAAAACAAGCCACTTTGGCAGTGC 1001  ${\tt nAspAsnGluGluArgLeuGlnValValLysLeuLeuAlaLysMetPheGlyAlaLysAspSerGluLeuAlaSerGlnAsnLysProLeuTrpGlnCys}$ 317 TACTTGGGCAGGTTTAATGATATCCATGTACCAATCCGCCTGGAATGTGTGAAATTTGCTAGCCATTGTCTCATGAACCATCCTGATTTAGCAAAAGACT 1101 TyrLeuGlyArgPheAsnAspIleHisValProIleArgLeuGluCysValLysPheAlaSerHisCysLeuMetAsnHisProAspLeuAlaLysAspL TAACAGAGTATCTTAAAGTGAGGTCACATGACCCTGAGGAAGCTATTAGACATGATGTTATTGTGTCAATAGTTACAGCTGCTAAAAAGGATATTCTTCT 1201 euThrGluTyrLeuLysValArgSerHisAspProGluGluAlaIleArgHisAspValIleValSerIleValThrAlaAlaLysLysAspIleLeuLe 384 GGTCAATGATCACTTACTTAATTTTGTGAGAGAGAGAACATTAGACAAACGATGGAGAGTACGCAAAGAAGCCATGATGGGACTTGCCCAAATTTATAAG 1301 uValAsnAspHisLeuLeuAsnPheValArgGluArgThrLeuAspLysArgTrpArgValArgLysGluAlaMetMetGlyLeuAlaGlnIleTyrLys 417 AAATATGCTTTACAGTCAGCAGCTGGAAAAGATGCTGCAAAACAGATAGCATGGATCAAAGACAAATTGCTACATATATTATCAAAATAGTATTGATG I 1401 LysTyrAlaLeuGlnSerAlaAlaGlyLysAspAlaAlaLysGlnIleAlaTrpIleLysAspLysLeuLeuHisIleTyrTyrGlnAsnSerIleAspA 451 uj ATCGACTACTTGTTGAACGGATCTTTGCTCAATACATGGTTCCTCACAATTTAGAAACTACAGAACGGATGAAATGCTTATATTACTTGTATGCCACACT 1501 spArgLeuLeuValGluArgIlePheAlaGlnTyrMetValProHisAsnLeuGluThrThrGluArgMetLysCysLeuTyrTyrLeuTyrAlaThrLe 484 **} +** GGATTTAAATGCTGTGAAAGCATTGAATGAAATGTGGAAATGTCAAAATCTGCTCCGACATCAAGTAAAGGATTTGCTTGACTTGATTAAGCAACCCAAA 1601 uAspLeuAsnAlaValLysAlaLeuAsnGluMetTrpLysCysGlnAsnLeuLeuArgHisGlnValLysAspLeuLeuAspLeuIleLysGlnProLys 517 ΠJ **41** 1701 ThrAspAlaSerValLysAlaIlePheSerLysValMetValIleThrArgAsnLeuProAspProGlyLysAlaGlnAspPheMetLysLysPheThrG 551 Ō) L 1801  ${\tt lnValLeuGluAspAspGluLysIleArgLysGlnLeuGluValLeuValSerProThrCysSerCysLysGlnAlaGluGlyCysValArgGluIleThroughluGluGluGlyCysValArgGluIleThroughluGluGlyCysValArgGluIleThroughluGluGlyCysValArgGluIleThroughluGluGlyCysValArgGluIleThroughluGluGlyCysValArgGluIleThroughluGluGlyCysValArgGluIleThroughluGluGlyCysValArgGluIleThroughluGluGlyCysValArgGluIleThroughluGluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluIleThroughluGlyCysValArgGluGlyCysValArgGluIleThroughluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGluGlyCysValArgGlyCysVa$ 584 TAAGAAGTTGGGCAACCCCAAACAGCCTACAAATCCTTTCCTGGAAATGATCAAGTTTCTCTTGGAGAGGATAGCACCTGTGCACATAGATACCGAATCT 1901 rLysLysLeuGlyAsnProLysGlnProThrAsnProPheLeuGluMetIleLysPheLeuLeuGluArgIleAlaProValHisIleAspThrGluSer C ATCAGTGCTCTTATTAAACAAGTGAACAAATCAATAGATGGAACAGCAGATGATGAAGATGAGGGTGTTCCAACTGATCAAGCCATCAGAGCAGGTCTTG N 2001 IleSerAlaLeuIleLysGlnValAsnLysSerIleAspGlyThrAlaAspAspGluAspGluGlyValProThrAspGlnAlaIleArgAlaGlyLeuG 651 ħ. AACTGCTTAAGGTACTCTCATTTACACATCCCATCTCATTTCATTCTGCTGAAACATTTGAATCATTACTGGCTTGTCTGAAAATGGATGAAAAAGT luLeuLeuLysValLeuSerPheThrHisProIleSerPheHisSerAlaGluThrPheGluSerLeuLeuAlaCysLeuLysMetAspAspGluLysVa 7= 684 2201 717 lAlaGluAlaAlaLeuGlnIlePheLysAsnThrGlySerLysIleGluGluAspPheProHisIleArgSerAlaLeuLeuProValLeuHisHisLys 2301 SerLysLysGlyProProArgGlnAlaLysTyrAlaIleHisCysIleHisAlaIlePheSerSerLysGluThrGlnPheAlaGlnIlePheGluProL 751 TGCATAAGAGCCTAGATCCAAGCCAACCTGGAACATCTCATAACACCATTGGTTACTATTGGTCATATTGCTCCTTGCACCTGATCAATTTGCTGCTCC euHisLysSerLeuAspProSerAsnLeuGluHisLeuIleThrProLeuValThrIleGlyHisIleAlaLeuLeuAlaProAspGlnPheAlaAlaPr 784 2501 oTrpLysSerTrpValAlaThrPheIleValLysAspLeuLeuMetAsnAspArgLeuProGlyLysLysThrThrLysLeuTrpValProAspGluGlu 817 GTATCTCCTGAGACAATGGTCAAAATTCAGGCTATTAAAATGATGGTTCGATGGCTACTTGGAATGAAAATAATCACAGTAAATCAGGAACTTCTACCT ValSerProGluThrMetValLysIleGlnAlaīleLysMetMetValArgTrpLeuLeuGlyMetLysAsnAsnHisSerLysSerGlyThrSerThrL 851 TAAGATTGCTAACAACAATATTGCATAGTGATGCAGACTTGACAGAACAGGGGGAAAATTAGTAAACCAGATATGTCACGTCTGAGACTTGCTGCTGGGAG 2701 euArgLeuLeuThrThrIleLeuHisSerAspGlyAspLeuThrGluGlnGlyLysIleSerLysProAspMetSerArgLeuArgLeuAlaAlaGlySe 884 TGCTATTGTGAAGCTGGCACAAGAACCCTGTTACCATGAAATCATCACATTAGAACAATATCAGCTATGTGCATTAGCTATCAACGATGAATGCTATCAA 2801 rAlaileValLysLeuAlaGlnGluProCysTyrHisGluIleIleThrLeuGluGlnTyrGlnLeuCysAlaLeuAlaileAsnAspGluCysTyrGln 917 GTAAGACAAGTGTTTGCCCAGAAACTTCACAAAGGCCTTTCCCGTTTACGGCTTCCACTTGAGTATATGGCAATCTGTGCCCTTTGTGCAAAAGATCCTG 2901 ValArgGlnValPheAlaGlnLysLeuHisLysGlyLeuSerArgLeuArgLeuProLeuGluTyrMetAlaIleCysAlaLeuCysAlaLysAspProV TAAAGGAGAGAGAGCTCATGCTAGGCAATGTTTGGTGAAAAATATAAATGTAAGGCGGGAGTATCTGAAGCAGCATGCAGCTGTTAGTGAAAAATTATT 95: alLysGluArgArgAlaHisAlaArgGlnCysLeuValLysAsnIleAsnValArgArgGluTyrLeuLysGlnHisAlaAlaValSerGluLysLeuLe  $\tt GTCTCTTCTACCAGAGTATGTTGTTCCATATACPATTCACCTTTTGGCACATGACCCAGATTATGTCAAAGTACAGGATATTGAACAACTTAAAGATGTT$ 3101 uSerLeuLeuProGluTyrValValProTyrThrIleHisLeuLeuAlaHisAspProAspTyrValLysValGlnAsplleGluGlnLeuLysAspVal 1017 3201

1053

